

SEQUENCE LISTING

<110> Chandrashekhar, Ramaswamy
Morales, Tony H.

<120> Parasitic Helminth Cuticlin Proteins, Nucleic Acid Molecules, and Uses Thereof

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<140> not yet assigned

<141> 1999-06-01

<150> 60/087,435

<151> 1998-06-01

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<170> PatentIn Ver. 2.0

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tgt gga cca act tca ata aca atc aat ttt aat aca cgt aat gca ttc 144
Cys Gly Pro Thr Ser Ile Thr Ile Asn Phe Asn Thr Arg Asn Ala Phe
35 40 45

gaa gga cat gtt tat gtg aaa ggt ctt tat gat caa gaa ggt tgc cgt 192
Glu Gly His Val Tyr Val Lys Gly Leu Tyr Asp Gln Glu Gly Cys Arg
50 55 60

aat gat gaa ggt gga cgt caa gtt gcc gga att tca ctt cca ttt gat 240
Asn Asp Glu Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp
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Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe
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gta aca aca act gtt gtc att tcg ttt cat cca tta ttt gtt acc aaa 336
Val Thr Thr Val Val Ile Ser Phe His Pro Leu Phe Val Thr Lys
100 105 110

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 115 120 125

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 180 185 190

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 195 200 205

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 aaa tat gcg gat cga tca cag ctt ttc tat caa tgc cag atc agt att 768
 Lys Tyr Ala Asp Arg Ser Gln Leu Phe Tyr Gln Cys Gln Ile Ser Ile
 245 250 255

 acc att aaa gaa cca aat agc gaa tgt gtt cga cca caa tgt tca gaa 816
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 cca caa gga ttc gga gct gtt aaa aca ggt ggt gcc gca gca aaa cct 864
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 275 280 285

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 35 40 45

 Glu Gly His Val Tyr Val Lys Gly Leu Tyr Asp Gln Glu Gly Cys Arg
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Gly Pro Thr Gly Gln Pro Val Gln Phe Ala Ile Ile Gly Gln Pro Val
165 170 175

Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala
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Val Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Thr Val Glu
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Ile Leu Asn Ala Asp Gly Cys Ala Leu Asp Lys Tyr Leu Leu Asn Asn
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Gln His Asn Gly Gln Pro Val Ile Leu Ala Ala Val Gln Asn Gly Ile
340 345 350

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Val Cys Arg Tyr Glu Ile Leu Glu Gly Gly Pro Thr Gly Ala Pro Val
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Arg Phe Ala Met Ile Gly Asp His Val Tyr His Lys Trp Thr Cys Asp
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 Ala Leu Asp Lys Tyr Leu Leu Asn Asn Leu Glu Tyr Ile Thr Asp Leu
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 130 135 140

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 Glu Cys Pro Arg Pro Gln Cys Thr Glu Pro Gln Gly Phe Gly Ala Ile
 145 150 155 160

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 Lys Ser Gly Gln Gly Phe Ala Ala Val Lys Ser Ala Ala Ala Pro Ala
 165 170 175

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 195 200 205

ata acc gaa gag aat ccg aac ttc tca gca aat cgt tta tca tca tca 672
 Ile Thr Glu Glu Asn Pro Asn Phe Ser Ala Asn Arg Leu Ser Ser Ser
 210 215 220

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 225 230 235 240

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Val Cys Arg Tyr Glu Ile Leu Glu Gly Gly Pro Thr Gly Ala Pro Val
35 40 45

Arg Phe Ala Met Ile Gly Asp His Val Tyr His Lys Trp Thr Cys Asp
50 55 60

Ser Glu Thr Thr Asp Thr Phe Cys Ala Leu Val His Ser Cys Val Val
65 70 75 80

Asp Asp Gly Lys Gly Asp Ala Val Glu Ile Leu Asn Glu Glu Gly Cys
85 90 95

Ala Leu Asp Lys Tyr Leu Leu Asn Asn Leu Glu Tyr Ile Thr Asp Leu
100 105 110

Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala Asp Arg Ser Glu
115 120 125

Leu Tyr Tyr Gln Cys Gln Ile Ser Ile Thr Ile Lys Glu Pro His Ser
130 135 140

Glu Cys Pro Arg Pro Gln Cys Thr Glu Pro Gln Gly Phe Gly Ala Ile
145 150 155 160

Lys Ser Gly Gln Gly Phe Ala Ala Val Lys Ser Ala Ala Ala Pro Ala
165 170 175

Pro Glu Ala Ser Leu Leu Ser Pro Arg Leu Ile Lys Lys Arg Ser Ile
180 185 190

Asn Ser Asp Asn Thr Val Asp Val Ser Thr Gly Phe Ser Thr Val Asp
195 200 205

Ile Thr Glu Glu Asn Pro Asn Phe Ser Ala Asn Arg Leu Ser Ser Ser
210 215 220

Thr Ser Arg Glu Gln Phe Asn Gly Ile Phe Cys Ile Ala Ser Asn Asp
225 230 235 240

Ile Leu Leu Ile Ile Leu Phe Gly Ala Met Leu Ala Ile Ala Cys Ile
245 250 255

Phe Phe Thr Ala Phe Leu Val His Ser Asn Asn His Ser Lys Ser
260 265 270

<210> 10

<211> 813

<212> DNA

<213> *Dirofilaria immitis*

<400> 10

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taacatagca ccgaacaaaa tgataagtaa aatatcattt gatcaatac agaagatacc 120

attgaattgt tcacggctcg ttgatgatga taaacgattt gctgagaagt tcggattctc 180

ttcggttata tcaaccgtgc taaaaccggt actgacgtcc accgtattat cagaattaat 240

tgatcgcttc ttgatcaatc gtggagaaag caaggaagct tctggagctg gtgcagcagc 300

agattttaca gcagcaaatc ctgtccaga ttttatggca ccaaattcattt gtggctctgt 360

gcatttgttgtt cgaggacatt cgctatgtgg ctctttaatt gttatactaa tctggcattt 420

atagtaaatcgt tctgatcgat ctgcataattt ataaacatga gcttcttggc cagccattaa 480

atctgtataa tattccaaat tattgagtaa atatttgtcc aaagcacatc cttcttcatt 540

cagaatctcc actgcatac cttttccatc atccacaaca catgaatgtt ctaatgcaca 600

gaatgtatct gtatgtctgtt aatcacatgtt ccatttgttatacatatgtt ctccaaatcat 660

tgcaaatcga acaggtgcac cagttggtcc accttccaaa atctcatatc gacatacggg 720

cattggtacc acttgagttt ggaatgctgtt agtcatttca gataacttcaa ggaccagtac 780

taacggtctt atcagcttc catataaaaaa cat

813

C O D E N T E R D A T A S E T

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 11
ggctggccaa gaagctcacg tatacaaata tgcg 34

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 12
cgcataattt gatacgtgag cttcttgcc agcc 34

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13
ggttaatta cccaagttt ag 22

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 14
ccatcctaat acgactcact atagggc

27

<210> 15
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 15
ggttatatca accgtgctaa aaccggtaact gacgtccacc g 41

<210> 16
<211> 892
<212> DNA
<213> Brugia malayi

<220>
<221> CDS
<222> (158)..(892)

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gcaatttcaa attaattcatt ttgctaattc tattattcca actattttca tcactaatca 120
ctgagaagaa atcaggaaga aagaagcaaa aagttaa atg ttg cat atg caa att 175
Met Leu His Met Gln Ile
1 5

tgc tca ttt ttg tca tat atg ata ata gca agt att aat gct att cca 223
Cys Ser Phe Leu Ser Tyr Met Ile Ile Ala Ser Ile Asn Ala Ile Pro
10 15 20

att gat aat ggt gtc gaa agt gaa cct gaa att gaa tgt ggt cca aca 271
Ile Asp Asn Gly Val Glu Ser Glu Pro Glu Ile Glu Cys Gly Pro Thr
25 30 35

tca atc act gtt aat ttt aat act cga aat cct ttt gaa gga cat gta 319
Ser Ile Thr Val Asn Phe Asn Thr Arg Asn Pro Phe Glu Gly His Val
40 45 50

tat gct aaa gga tta tac agt aat caa gat tgt cgt agt gat gaa ggt 367

Tyr Ala Lys Gly Leu Tyr Ser Asn Gln Asp Cys Arg Ser Asp Glu Gly
 55 60 65 70 415
 gga cgt cag gta gcc gga ata tca tta ccg ttt gat tca tgt aat gtc
 Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp Ser Cys Asn Val
 75 80 85 463
 gca cgt aca cgt tcg tta aat cca cgt gga ata ttt gtc aca gct gtt
 Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe Val Thr Ala Val
 90 95 100 511
 gtg gta att acg ttt cat cca cag ttt atc aca aaa gtt gat cga aca
 Val Val Ile Thr Phe His Pro Gln Phe Ile Thr Lys Val Asp Arg Thr
 105 110 115 559
 tat cga ttg caa tgc ttt tac atg gaa gct gat aag act gtt agc aca
 Tyr Arg Leu Gln Cys Phe Tyr Met Glu Ala Asp Lys Thr Val Ser Thr
 120 125 130 607
 caa att gaa gtt tcc gaa atg aca acc gta ttt gct aca caa ttg gta
 Gln Ile Glu Val Ser Glu Met Thr Val Phe Ala Thr Gln Leu Val
 135 140 145 150 655
 cca atg cct gtg tgt aga tat gag att ctg gat ggt ggt cca acc gga
 Pro Met Pro Val Cys Arg Tyr Glu Ile Leu Asp Gly Gly Pro Thr Gly
 155 160 165 703
 caa cct gtc cag tat gct aat att gga caa ccg gtt tat cat aaa tgg
 Gln Pro Val Gln Tyr Ala Asn Ile Gly Gln Pro Val Tyr His Lys Trp
 170 175 180 751
 aca tgt gat tct gaa aca gtt gat acc ttc tgt gct ttg gta cat tcc
 Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala Leu Val His Ser
 185 190 195 799
 tgt ttt gtt gat gat ggc aat ggt gac agt att aat tta att aat gaa
 Cys Phe Val Asp Asp Gly Asn Gly Asp Ser Ile Asn Leu Ile Asn Glu
 200 205 210 847
 gaa gga tgt gca tta gat cga tat ctt cta aat aat ttg gaa tat cca
 Glu Gly Cys Ala Leu Asp Arg Tyr Leu Leu Asn Asn Leu Glu Tyr Pro
 215 220 225 230 892
 act gat cta atg gct ggc caa gaa gct cac gta tac aaa tat gcg
 Thr Asp Leu Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala
 235 240 245

<210> 17
<211> 245
<212> PRT
<213> Brugia malayi

<400> 17
 Met Leu His Met Gln Ile Cys Ser Phe Leu Ser Tyr Met Ile Ile Ala
 1 5 10 15
 Ser Ile Asn Ala Ile Pro Ile Asp Asn Gly Val Glu Ser Glu Pro Glu
 20 25 30
 Ile Glu Cys Gly Pro Thr Ser Ile Thr Val Asn Phe Asn Thr Arg Asn
 35 40 45
 Pro Phe Glu Gly His Val Tyr Ala Lys Gly Leu Tyr Ser Asn Gln Asp
 50 55 60
 Cys Arg Ser Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro
 65 70 75 80
 Phe Asp Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly
 85 90 95
 Ile Phe Val Thr Ala Val Val Val Ile Thr Phe His Pro Gln Phe Ile
 100 105 110
 Thr Lys Val Asp Arg Thr Tyr Arg Leu Gln Cys Phe Tyr Met Glu Ala
 115 120 125
 Asp Lys Thr Val Ser Thr Gln Ile Glu Val Ser Glu Met Thr Thr Val
 130 135 140
 Phe Ala Thr Gln Leu Val Pro Met Pro Val Cys Arg Tyr Glu Ile Leu
 145 150 155 160
 Asp Gly Gly Pro Thr Gly Gln Pro Val Gln Tyr Ala Asn Ile Gly Gln
 165 170 175
 Pro Val Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe
 180 185 190
 Cys Ala Leu Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Ser
 195 200 205
 Ile Asn Leu Ile Asn Glu Glu Gly Cys Ala Leu Asp Arg Tyr Leu Le
 210 215 220

Asn Asn Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His
225 230 235 240

Val Tyr Lys Tyr Ala
245

INS BI

<210> 18
<211> 892
<212> DNA
<213> Brugia malayi

<400> 18
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attgccatca tcaacaaaac aggaatgtac caaagcacag aaggtatcaa ctgtttcaga 180
atcacatgtc catttatgt aaaccggttg tccaatatta gcatactgga caggttgtcc 240
ggttggacca ccatccagaa tctcatatct acacacaggg attggtacca attgtgtac 300
aaatacggtt gtcatttcgg aaacttcaat ttgtgtgcta acagtcttat cagttccat 360
gtaaaaagcat tgcaatcgat atgttcgatc aactttgtg ataaaactgtg gatgaaacgt 420
aattaccaca acagctgtga caaatattcc acgtggattt aacgaaacgtg tacgtgcgac 480
attacatgaa tcaaacggta atgatattcc ggctacctga cgtccacctt catcaactacg 540
acaatcttga ttactgtata atcctttagc atatacatgt cttccaaag gatttcgagt 600
attaaaatta acagtgattt atgttggacc acattcaatt tcaggttcac ttgcacacc 660
attatcaatt ggaatagcat taatacttgc tattatcata tatgacaaaa atgagcaaatt 720
ttgcataatgc aacatttaac ttttgcttc tttttcctg atttcttc acgtgattt 780
gatgaaaaata gttgaaataa tagaatttgc aaaatgatta atttggaaatt gcaacaaatt 840
attgaattat tgatgatcaa ttttaatgtat ctcacacttg ggttaattttt cc 892